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► To cite this version:

Christel Marie-Etancelin, Suzanne Rowe, Arjan Jonker, Annabelle Meynadier. Genetic approach of rumen metagenome: state of the art in small ruminant and perspectives. 69. Annual Meeting of the European Federation of Animal Science (EAAP), Aug 2018, Dubrovnik, Croatia. 705 p. hal-02737387

HAL Id: hal-02737387

<https://hal.inrae.fr/hal-02737387>

Submitted on 2 Jun 2020

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Genetic approach of rumen metagenome: state of the art in small ruminant and perspectives

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The ruminal microbiome plays a central role in the nutrition of the ruminant host, directly affecting production and undesirable by-products such as methane. Studies on ruminal microbiota highlight a significant effect of the host, but few publications have reported results concerning the impact of host genetics on microbial community composition.

Rumen microbiota can be described using targeted or whole genome sequencing: rRNA is primarily used for the determination of taxonomic abundance of bacteria/archaea/fungi/protozoa, and a shotgun approach for abundance of genes in the rumen. An alternative high-throughput genotyping by sequencing technique was recently proposed by Hess et al. (2018) for describing microbial community composition in large numbers of animals. In sheep, a comparison of extreme animals (phenotypically or genetically) showed differences in their microbiota. Ellison et al. (2017) reported differences in bacteria and archaea abundances in sheep having low or high residual feed intake, with some interactions with the diet. There was little evidence of links between feeding rate in sheep and ruminal bacteria abundances (Etancelin et al., 2018). From divergent lines, Kittelmann et al. (2014) showed 3 bacterial community types linked with genetic level of methane emission and de Barbieri et al. (2015) reported that selection for fleece weight is associated with differences in the diversity of ruminal bacteria. The first estimates of microbiota heritabilities in sheep were provided by Rowe et al. (2015) who reported genetic control of rumen microbial communities and genetic links to methane emissions. For this conference, Marie-Etancelin et al. (2018) estimated that $\frac{1}{4}$ of the taxa genera abundances in the rumen have a heritability greater than 0.1. It would be useful if these preliminary results on the targeted metagenome approach were followed up by whole gene quantification to characterize the functionality of microbiota. As in cattle (Difford et al., 2018), microbiota metagenome and host's genome contributions to the variability of traits should be considered simultaneously in sheep experiments.